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ABSTRACT

The present invention provides [A]] high throughput mutagenesis screening methods utilizing *Pseudomonas mendocina* cutinase. In preferred embodiments, the methods of the present invention involve selection[s] of sites for saturation scanning using protein structural considerations. Site-saturation libraries are created and screened using assays for sites having protein properties of interest. The sites are categorized for the properties of interest, trends, if any, are identified; and, a variant having a desired property is selected for additional library creation procedures. The additional libraries are created using feedback from the determined categories. One set of additional libraries repeats construction of the previous libraries using the feedback. A second set of additional libraries are new libraries created at sites that are expected to be beneficial based on the feedback. The categories may be coded, using color or other indicia, to allow easy identification of trends.

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